RAW SEQUENCE LISTING   DATE: 08/28/2001
PATENT APPLICATION: **US/09/628,693**   TIME: 08:20:34

Input Set : **A:\34950193.app**
Output Set: N:\CRF3\08282001\I628693.raw

```
 3  <110> APPLICANT: Haroche, Julien
 4         Allignet, Jeanine
 5         El Solh, Nevine
 7  <120> TITLE OF INVENTION: DETECTION OF A GENE, vatD, ENCODING AN ACETYLTRANSFERASE
 8         INACTIVATING STREPTOGRAMIN
10  <130> FILE REFERENCE: 03495.0193
12  <140> CURRENT APPLICATION NUMBER: US/09/628,693
13  <141> CURRENT FILING DATE: 2000-07-28
15  <160> NUMBER OF SEQ ID NOS: 22
17  <170> SOFTWARE: PatentIn Ver. 2.1
19  <210> SEQ ID NO: 1
20  <211> LENGTH: 213
21  <212> TYPE: PRT
22  <213> ORGANISM: Enterococcus faecium
24  <400> SEQUENCE: 1
25  Met Thr Ile Pro Asp Ala Asn Ala Ile Tyr His Asn Ser Ala Ile Lys
26   1               5                  10                  15
28  Glu Val Val Phe Ile Lys Asn Val Ile Lys Ser Pro Asn Ile Glu Ile
29                  20                  25                  30
31  Gly Asp Tyr Thr Tyr Tyr Asp Asp Pro Val Asn Pro Thr Asp Phe Glu
32              35                  40                  45
34  Lys His Val Thr His His Tyr Glu Phe Leu Gly Asp Lys Leu Ile Ile
35          50                  55                  60
37  Gly Lys Phe Cys Ser Leu Ala Ser Gly Ile Glu Phe Ile Met Asn Gly
38   65                  70                  75                  80
40  Ala Asn His Val Met Lys Gly Ile Ser Thr Tyr Pro Phe Asn Ile Leu
41                  85                  90                  95
43  Gly Gly Asp Trp Gln Gln Tyr Thr Pro Glu Leu Thr Asp Leu Pro Leu
44              100                 105                 110
46  Lys Gly Asp Thr Val Val Gly Asn Asp Val Trp Phe Gly Gln Asn Val
47          115                 120                 125
49  Thr Val Leu Pro Gly Val Lys Ile Gly Asp Gly Ala Ile Ile Gly Ala
50          130                 135                 140
52  Asn Ser Val Val Thr Lys Asp Val Ala Pro Tyr Thr Ile Val Gly Gly
53  145                 150                 155                 160
55  Asn Pro Ile Gln Leu Ile Gly Pro Arg Phe Glu Pro Glu Val Ile Gln
56                  165                 170                 175
58  Ala Leu Glu Asn Leu Ala Trp Trp Asn Lys Asp Ile Glu Trp Ile Thr
59              180                 185                 190
61  Ala Asn Val Pro Lys Leu Met Gln Thr Thr Pro Thr Leu Glu Leu Ile
62          195                 200                 205
64  Asn Ser Leu Met Glu
65      210
68  <210> SEQ ID NO: 2
69  <211> LENGTH: 642
70  <212> TYPE: DNA
71  <213> ORGANISM: Enterococcus faecium
```

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73 <400> SEQUENCE: 2
74 atgactatac ctgacgcaaa tgcaatctat cataactcag ccatcaaaga ggttgtcttt 60
75 atcaagaacg tgatcaaaag tcccaatatt gaaattgggg actacaccta ttatgatgac 120
76 ccagtaaatc ccaccgattt tgagaaacac gttacccatc actatgaatt tctaggcgac 180
77 aaattaatca tcggtaaatt ttgttctctc gccagtggca ttgaatttat catgaacggt 240
78 gccaaccacg taatgaaagg tatttcgact tatccattta atatattagg tggcgattgg 300
79 caacaataca ctcctgaact gactgatttg ccgttgaaag gtgatactgt agtcggaaat 360
80 gacgtgtggt ttgggcaaaa tgtgaccgtc ctaccaggcg taaaaatagg tgacggtgcc 420
81 attatcggag caaatagtgt tgtaacaaaa gacgtcgctc catatacaat tgtcggtggc 480
82 aatccaattc aactcatcgg accaagattt gaaccggaag ttattcaagc attagaaaat 540
83 ctggcatggt ggaataaaga tattgaatgg ataactgcta atgttcctaa actaatgcaa 600
84 acaacaccca cacttgaatt gataaacagt ttaatggaaa aa                    642
87 <210> SEQ ID NO: 3
88 <211> LENGTH: 25
89 <212> TYPE: DNA
90 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
95 <400> SEQUENCE: 3
96 caatattgga attcgggact acacc                                       25
99 <210> SEQ ID NO: 4
100 <211> LENGTH: 22
101 <212> TYPE: DNA
102 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
107 <400> SEQUENCE: 4
108 ctgtttatga attcaagtgt gg                                          22
111 <210> SEQ ID NO: 5
112 <211> LENGTH: 7
113 <212> TYPE: PRT
114 <213> ORGANISM: Enterococcus faecium
116 <400> SEQUENCE: 5
117 Ile Met Asn Gly Ala Asn His
118    1              5
121 <210> SEQ ID NO: 6
122 <211> LENGTH: 18
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial Sequence
126 <220> FEATURE:
127 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
129 <220> FEATURE:
130 <223> OTHER INFORMATION: "n" bases may be a, t, c or g
132 <400> SEQUENCE: 6
133 athatgaayg cnaaycay                                               18
136 <210> SEQ ID NO: 7
137 <211> LENGTH: 5
138 <212> TYPE: PRT
139 <213> ORGANISM: Enterococcus faecium
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141 <400> SEQUENCE: 7
142 Gly Asn Asp Val Trp
143   1                 5
146 <210> SEQ ID NO: 8
147 <211> LENGTH: 15
148 <212> TYPE: DNA
149 <213> ORGANISM: Artificial Sequence
151 <220> FEATURE:
152 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
154 <220> FEATURE:
155 <223> OTHER INFORMATION: "n" bases may be a, t, c or g
157 <400> SEQUENCE: 8
158 ccanacrtcr ttncc                                                  15
161 <210> SEQ ID NO: 9
162 <211> LENGTH: 8
163 <212> TYPE: PRT
164 <213> ORGANISM: Enterococcus faecium
166 <400> SEQUENCE: 9
167 Ala Asn Ala Ile Tyr His Asn Ser
168   1                 5
171 <210> SEQ ID NO: 10
172 <211> LENGTH: 24
173 <212> TYPE: DNA
174 <213> ORGANISM: Enterococcus faecium
176 <400> SEQUENCE: 10
177 gcaaatgcaa tctatcataa ctca                                        24
180 <210> SEQ ID NO: 11
181 <211> LENGTH: 9
182 <212> TYPE: PRT
183 <213> ORGANISM: Enterococcus faecium
185 <400> SEQUENCE: 11
186 Met Gln Thr Thr Pro Thr Leu Glu Leu
187   1                 5
190 <210> SEQ ID NO: 12
191 <211> LENGTH: 27
192 <212> TYPE: DNA
193 <213> ORGANISM: Enterococcus faecium
195 <400> SEQUENCE: 12
196 atgcaaacaa cacccacact tgaattg                                     27
199 <210> SEQ ID NO: 13
200 <211> LENGTH: 23
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence
204 <220> FEATURE:
205 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
207 <400> SEQUENCE: 13
208 tagaaagaat tcagtgattg tgg                                         23
211 <210> SEQ ID NO: 14
212 <211> LENGTH: 26
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213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
217 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
219 <400> SEQUENCE: 14
220 ggattcacta aatagtaaag gccgtg                                    26
223 <210> SEQ ID NO: 15
224 <211> LENGTH: 840
225 <212> TYPE: DNA
226 <213> ORGANISM: Enterococcus faecium
228 <400> SEQUENCE: 15
229 aaatttaggc gcacaaaaag aaagagtgtg acaaaacatg gttatgctac atgtttaagg 60
230 taaaaatagt tatgtcacaa ctacttattt ttttacccaa tcttctagac tataattaaa 120
231 attaaataac tcaattcgga ggtactaacc tgactatacc tgacgcaaat gcaatctatc 180
232 ataactcagc catcaaagag gttgactttta tcaagaacgt gatcaaaagt cccaatattg 240
233 aaattgggga ctacacctat tatgatgacc cagtaaatcc caccgatttt gagaaacacg 300
234 ttacccatca ctatgaattt ctaggcgaca aattaatcat cggtaaattt tgttctctcg 360
235 ccagtggcat tgaatttatc atgaacggtg ccaaccacgt aatgaaaggt atttcgactt 420
236 atccatttaa tatattaggt ggcgattggc aacaatacac tcctgaactg actgatttgc 480
237 cgttgaaagg tgatactgta gtcggaaatg acgtgtggtt tgggcaaaat gtgaccgtcc 540
238 taccaggcgt aaaaataggt gacggtgcca ttatcggagc aaatagtgtt gtaacaaaag 600
239 acgtcgctcc atatacaatt gtcggtggca atccaattca actcatcgga ccaagatttg 660
240 aaccggaagt tattcaagca ttagaaaatc tggcatggtg gaataaagat attgaatgga 720
241 taactgctaa tgttcctaaa ctaatgcaaa caacacccac acttgaattg ataaacagtt 780
242 taatggaaaa ataaaaacaa aaaagccgtg caagcaatcc aaaaatgatt gtttacacgg 840
245 <210> SEQ ID NO: 16
246 <211> LENGTH: 44
247 <212> TYPE: DNA
248 <213> ORGANISM: Enterococcus faecium
250 <400> SEQUENCE: 16
251 tgtcacaact acttattttt ttacccaatc ttctagacta taat                44
254 <210> SEQ ID NO: 17
255 <211> LENGTH: 1080
256 <212> TYPE: DNA
257 <213> ORGANISM: Enterococcus faecium
259 <220> FEATURE:
260 <221> NAME/KEY: CDS
261 <222> LOCATION: (271)..(912)
263 <400> SEQUENCE: 17
264 ccctttaaag agggctttta tatattaatc acaaatcact tatcacaaat cacaagtgat 60
266 ttgtgattgt tgatgataaa ataagaataa gaagaaatag aaagaagtga gtgattgtgg 120
268 gaaatttagg cgcacaaaaa gaaagagtgt gacaaaacat ggttatgcta catgtttaag 180
270 gtaaaaatag ttatgtcaca actacttatt tttttaccca atcttctaga ctataattaa 240
272 aattaaataa ctcaattcgg aggtactaac atg act ata cct gac gca aat gca 294
273                                    Met Thr Ile Pro Asp Ala Asn Ala
274                                     1               5
276 atc tat cat aac tca gcc atc aaa gag gtt gtc ttt atc aag aac gtg 342
277 Ile Tyr His Asn Ser Ala Ile Lys Glu Val Val Phe Ile Lys Asn Val
278     10                  15                  20
```

```
280 atc aaa agt ccc aat att gaa att ggg gac tac acc tat tat gat gac   390
281 Ile Lys Ser Pro Asn Ile Glu Ile Gly Asp Tyr Thr Tyr Tyr Asp Asp
282  25                  30                  35                  40
284 cca gta aat ccc acc gat ttt gag aaa cac gtt acc cat cac tat gaa   438
285 Pro Val Asn Pro Thr Asp Phe Glu Lys His Val Thr His His Tyr Glu
286                  45                  50                  55
288 ttt cta ggc gac aaa tta atc atc ggt aaa ttt tgt tct ctc gcc agt   486
289 Phe Leu Gly Asp Lys Leu Ile Ile Gly Lys Phe Cys Ser Leu Ala Ser
290                  60                  65                  70
292 ggc att gaa ttt atc atg aac ggt gcc aac cac gta atg aaa ggt att   534
293 Gly Ile Glu Phe Ile Met Asn Gly Ala Asn His Val Met Lys Gly Ile
294             75                  80                  85
296 tcg act tat cca ttt aat ata tta ggt ggc gat tgg caa caa tac act   582
297 Ser Thr Tyr Pro Phe Asn Ile Leu Gly Gly Asp Trp Gln Gln Tyr Thr
298             90                  95                  100
300 cct gaa ctg act gat ttg ccg ttg aaa ggt gat act gta gtc gga aat   630
301 Pro Glu Leu Thr Asp Leu Pro Leu Lys Gly Asp Thr Val Val Gly Asn
302 105                 110                 115                 120
304 gac gtg tgg ttt ggg caa aat gtg acc gtc cta cca ggc gta aaa ata   678
305 Asp Val Trp Phe Gly Gln Asn Val Thr Val Leu Pro Gly Val Lys Ile
306                 125                 130                 135
308 ggt gac ggt gcc att atc gga gca aat agt gtt gta aca aaa gac gtc   726
309 Gly Asp Gly Ala Ile Ile Gly Ala Asn Ser Val Val Thr Lys Asp Val
310                 140                 145                 150
312 gct cca tat aca att gtc ggt ggc aat cca att caa ctc atc gga cca   774
313 Ala Pro Tyr Thr Ile Val Gly Gly Asn Pro Ile Gln Leu Ile Gly Pro
314             155                 160                 165
316 aga ttt gaa ccg gaa gtt att caa gca tta gaa aat ctg gca tgg tgg   822
317 Arg Phe Glu Pro Glu Val Ile Gln Ala Leu Glu Asn Leu Ala Trp Trp
318         170                 175                 180
320 aat aaa gat att gaa tgg ata act gct aat gtt cct aaa cta atg caa   870
321 Asn Lys Asp Ile Glu Trp Ile Thr Ala Asn Val Pro Lys Leu Met Gln
322 185                 190                 195                 200
324 aca aca ccc aca ctt gaa ttg ata aac agt tta atg gaa aaa           912
325 Thr Thr Pro Thr Leu Glu Leu Ile Asn Ser Leu Met Glu Lys
326                 205                 210
328 taaaaacaaa aaagccgtgc aagcaatcca aaaatgattg tttacacggc ctttactatt 972
330 tagtgaatcc aatttattaa taatagatat gatataccag taaaaaatac actagccacc 1032
332 tctggcggta ctctactcgt atattttatt tacgaccttc tgatgata              1080
335 <210> SEQ ID NO: 18
336 <211> LENGTH: 214
337 <212> TYPE: PRT
338 <213> ORGANISM: Enterococcus faecium
340 <400> SEQUENCE: 18
341 Met Thr Ile Pro Asp Ala Asn Ala Ile Tyr His Asn Ser Ala Ile Lys
342  1               5                   10                  15
344 Glu Val Val Phe Ile Lys Asn Val Ile Lys Ser Pro Asn Ile Glu Ile
345             20                  25                  30
347 Gly Asp Tyr Thr Tyr Tyr Asp Asp Pro Val Asn Pro Thr Asp Phe Glu
```

VERIFICATION SUMMARY   DATE: 08/28/2001
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```
L:12  M:270 C: Current Application Number differs, Replaced Application Number
L:13  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:133 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:133 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:158 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:158 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
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